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SEQUENCE LISTING

<110> Japan as represented by Director-General of Agency of Industrial Science and Technology

<120> A thermostable enzyme having aminotransferase activity and a gene coding the enzyme

<130> PH-640-PCT

<160> 2

<210> 1

<211> 389

<212> PRT

<213> Pyrococcus horikoshi

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30

Ile Gly Glu Pro Asp Phe Asp Thr Pro Gln His Ile Lys Glu Tyr Ala

35

40

45

Lys Glu Ala Leu Asp Lys Gly Leu Thr His Tyr Gly Pro Asn Ile Gly

50

55

60

Leu Leu Glu Leu Arg Glu Ala Ile Ala Glu Lys Leu Lys Lys Gln Asn

65 70 75 80

Gly Ile Glu Ala Asp Pro Lys Thr Glu Ile Met Val Leu Leu Gly Ala

85 90 95

Asn Gln Ala Phe Leu Met Gly Leu Ser Ala Phe Leu Lys Asp Gly Glu

100 105 110

Glu Val Leu Ile Pro Thr Pro Ala Phe Val Ser Tyr Ala Pro Ala Val

115 120 125

Ile Leu Ala Gly Gly Lys Pro Val Glu Val Pro Thr Tyr Glu Glu Asp

130 135 140

Glu Phe Arg Leu Asn Val Asp Glu Leu Lys Lys Tyr Val Thr Asp Lys

145 150 155 160

Thr Arg Ala Leu Ile Ile Asn Ser Pro Cys Asn Pro Thr Gly Ala Val

165 170 175

Leu Thr Lys Lys Asp Leu Glu Glu Ile Ala Asp Phe Val Val Glu His

180 185 190

Asp Leu Ile Val Ile Ser Asp Glu Val Tyr Glu His Phe Ile Tyr Asp

195 200 205

Asp Ala Arg His Tyr Ser Ile Ala Ser Leu Asp Gly Met Phe Glu Arg

210

215

220

Thr Ile Thr Val Asn Gly Phe Ser Lys Thr Phe Ala Met Thr Gly Trp

225

230

235

240

Arg Leu Gly Phe Val Ala Ala Pro Ser Trp Ile Ile Glu Arg Met Val

245

250

255

Lys Phe Gln Met Tyr Asn Ala Thr Cys Pro Val Thr Phe Ile Gln Tyr

260

265

270

Ala Ala Ala Lys Ala Leu Lys Asp Glu Arg Ser Trp Lys Ala Val Glu

275

280

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Glu Met Arg Lys Glu Tyr Asp Arg Arg Arg Lys Leu Val Trp Lys Arg

290

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300

Leu Asn Glu Met Gly Leu Pro Thr Val Lys Pro Lys Gly Ala Phe Tyr

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310

315

320

Ile Phe Pro Arg Ile Arg Asp Thr Gly Leu Thr Ser Lys Lys Phe Ser

325

330

335

Glu Leu Met Leu Lys Glu Ala Arg Val Ala Val Val Pro Gly Ser Ala

340

345

350

Phe Gly Lys Ala Gly Glu Gly Tyr Val Arg Ile Ser Tyr Ala Thr Ala

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Glu Arg Lys Leu Val

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<212> DNA

<213> Pyrococcus horikoshi

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Lys Leu Phe Asp Ile Ala Ala Gly Met Lys Asp Val Ile Ser Leu Gly

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ata ggg gaa cct gat ttt gat acg cct caa cat att aag gag tat gcc 144

Ile Gly Glu Pro Asp Phe Asp Thr Pro Gln His Ile Lys Glu Tyr Ala

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Lys Glu Ala Leu Asp Lys Gly Leu Thr His Tyr Gly Pro Asn Ile Gly

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Leu Leu Glu Leu Arg Glu Ala Ile Ala Glu Lys Leu Lys Lys Gln Asn

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Gly Ile Glu Ala Asp Pro Lys Thr Glu Ile Met Val Leu Leu Gly Ala

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90

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aac caa gct ttc tta atg ggc ctc tcg gct ttt ctt aag gat ggt gaa 336

Asn Gln Ala Phe Leu Met Gly Leu Ser Ala Phe Leu Lys Asp Gly Glu

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Glu Val Leu Ile Pro Thr Pro Ala Phe Val Ser Tyr Ala Pro Ala Val

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Ile Leu Ala Gly Gly Lys Pro Val Glu Val Pro Thr Tyr Glu Glu Asp

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gaa ttc agg cta aac gtt gat gag ctt aaa aag tat gtt acc gac aag 480

Glu Phe Arg Leu Asn Val Asp Glu Leu Lys Lys Tyr Val Thr Asp Lys

145

150

155

160

act aga gct tta ata ata aac tca ccg tgt aat cca acg gga gca gtc 528

Thr Arg Ala Leu Ile Ile Asn Ser Pro Cys Asn Pro Thr Gly Ala Val

165

170

175

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Leu Thr Lys Lys Asp Leu Glu Glu Ile Ala Asp Phe Val Val Glu His

gat cta att gta ata agc gat gaa gtt tat gag cac ttc att tac gat 624

Asp Leu Ile Val Ile Ser Asp Glu Val Tyr Glu His Phe Ile Tyr Asp

195

200

205

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Asp Ala Arg His Tyr Ser Ile Ala Ser Leu Asp Gly Met Phe Glu Arg

210

215

220

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Thr Ile Thr Val Asn Gly Phe Ser Lys Thr Phe Ala Met Thr Gly Trp

225

230

235

240

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Arg Leu Gly Phe Val Ala Ala Pro Ser Trp Ile Ile Glu Arg Met Val

245

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Lys Phe Gln Met Tyr Asn Ala Thr Cys Pro Val Thr Phe Ile Gln Tyr

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Ala Ala Ala Lys Ala Leu Lys Asp Glu Arg Ser Trp Lys Ala Val Glu

275

280

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Glu Met Arg Lys Glu Tyr Asp Arg Arg Arg Lys Leu Val Trp Lys Arg

290

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 Leu Asn Glu Met Gly Leu Pro Thr Val Lys Pro Lys Gly Ala Phe Tyr
 305 310 315 320

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 Ile Phe Pro Arg Ile Arg Asp Thr Gly Leu Thr Ser Lys Lys Phe Ser
 325 330 335

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 Glu Leu Met Leu Lys Glu Ala Arg Val Ala Val Val Pro Gly Ser Ala
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 Phe Gly Lys Ala Gly Glu Gly Tyr Val Arg Ile Ser Tyr Ala Thr Ala
 355 360 365

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 Tyr Glu Lys Leu Glu Glu Ala Met Asp Arg Met Glu Arg Val Leu Lys
 370 375 380

gag agg aag cta gtt taa 1170
 Glu Arg Lys Leu Val
 385 389